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OM protein - protein search, using sw model

Run on: January 31, 2005, 18:10:30 ; Search time 28 Seconds

(without alignments)  
48.108 Million cell updates/sec

Title: US-10-083-768-12

Perfect score: 85

Sequence: CADGPTLREWISFC 14

Scoring table: BL05162 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	52.9	108	2 T19731	hypothetical protein
2	44	51.8	974	2 S34189	starch phosphoryla
3	44	51.8	1022	1 S00503	Na+/K+-exchanging
4	44	51.8	1023	2 A24414	Na+/K+-exchanging
5	43	50.6	245	2 T47701	translation initia
6	43	50.6	490	2 T09084	phosphatidylinosit
7	43	50.6	1010	2 B37227	Na+/K+-exchanging
8	43	50.6	1013	1 S00801	Na+/K+-exchanging
9	43	50.6	1013	2 C04639	Na+/K+-exchanging
10	43	50.6	1017	2 A37227	Na+/K+-exchanging
11	43	50.6	1020	2 A34474	Na+/K+-exchanging
12	43	50.6	1020	2 B24639	Na+/K+-exchanging
13	43	50.6	1021	1 PWSHNA	Na+/K+-exchanging
14	43	50.6	1021	1 S04639	Na+/K+-exchanging
15	43	50.6	1021	2 A28199	Na+/K+-exchanging
16	43	50.6	1021	2 B24862	Na+/K+-exchanging
17	43	50.6	1022	2 S49127	Na+/K+-exchanging
18	43	50.6	1023	1 A24639	Na+/K+-exchanging
19	43	50.6	1023	1 S24650	Na+/K+-exchanging
20	43	50.6	1025	2 A0444	Na+/K+-exchanging
21	43	50.6	1027	1 PNCNM	Na+/K+-exchanging
22	43	50.6	1038	1 S03632	Na+/K+-exchanging
23	42.5	50.0	1004	2 JH0470	Na+/K+-exchanging
24	42	49.4	312	2 F86876	hypothetical protein
25	42	49.4	522	2 D59226	probable membrane
26	42	49.4	522	2 S62941	conserved hypothetical
27	42	49.4	725	2 A11544	starch phosphoryla
28	42	49.4	842	2 T12091	hypothetical prote
29	41	48.2	189	2 S07755	

#### ALIGNMENTS

RESULT 1									
T49731 hypothetical protein B24B19.30 [Imported] - Neurospora crassa									
C;Species: Neurospora crassa									
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000									
C;Accession: T49731									
R;Schulte, U.; Aign, V.; Hohensel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, A;Submitted to the Protein Sequence Database, May 2000									
A;Reference number: Z25022									
A;Accession: T49731									
A;Status: preliminary									
A;Molecule type: DNA									
A;Residues: 1-108 <SCH>									
A;Cross-references: EMBL:AL356192; GSPDB:GN00116; NCSP:B24B19.30									
A;Experimental source: BAC clone B24B19; strain OR74A									
C;Genetics:									
C;Map position: 6									
C;Superfamily: Neurospora crassa hypothetical protein B24B19.30									
Query Match									
C;Species: Solanum tuberosum (potato)									
C;Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004									
C;Accession: S53489; S34189									
R;Sonnewald, U.; Basner, A.; Greve, B.; Steup, M.									
Plant Mol. Biol. 27, 567-576, 1995									
A;Title: A second L-type isotype of potato glucan phosphorylase: cloning, antisense inhi									
A;Reference number: S53489; PMID:9520149; PMID:7894019									
A;Accession: S53489									
A;Status: nucleic acid sequence not shown									
A;Molecule type: mRNA									
A;Residues: 1-974 <S02>									
A;Cross-references: UNIPROT: P53535; EMBL:X73684; PID:9313348; PID:93133									
C;Superfamily: Glucan phosphorylase									
C;Keywords: Glycosyltransferase; hexosyltransferase; phosphoprotein; pyridoxal phosphate (Lys) (covalent) #status predicted									
F;820/Binding site: pyridoxal phosphate (Lys)									
Query Match									
C;Species: Solanum tuberosum (potato)									
C;Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004									
C;Accession: S53489; S34189									
R;Sonnewald, U.; Basner, A.; Greve, B.; Steup, M.									
Plant Mol. Biol. 27, 567-576, 1995									
A;Title: A second L-type isotype of potato glucan phosphorylase: cloning, antisense inhi									
A;Reference number: S53489; PMID:9520149; PMID:7894019									
A;Accession: S53489									
A;Status: nucleic acid sequence not shown									
A;Molecule type: mRNA									
A;Residues: 1-974 <S02>									
A;Cross-references: UNIPROT: P53535; EMBL:X73684; PID:9313348; PID:93133									
C;Superfamily: Glucan phosphorylase									
C;Keywords: Glycosyltransferase; hexosyltransferase; phosphoprotein; pyridoxal phosphate (Lys) (covalent) #status predicted									
F;820/Binding site: pyridoxal phosphate (Lys)									
Query Match									
C;Species: Solanum tuberosum (potato)									
C;Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004									
C;Accession: S53489; S34189									
R;Sonnewald, U.; Basner, A.; Greve, B.; Steup, M.									
Plant Mol. Biol. 27, 567-576, 1995									
A;Title: A second L-type isotype of potato glucan phosphorylase: cloning, antisense inhi									
A;Reference number: S53489; PMID:9520149; PMID:7894019									
A;Accession: S53489									
A;Status: nucleic acid sequence not shown									
A;Molecule type: mRNA									
A;Residues: 1-974 <S02>									
A;Cross-references: UNIPROT: P53535; EMBL:X73684; PID:9313348; PID:93133									
C;Superfamily: Glucan phosphorylase									
C;Keywords: Glycosyltransferase; hexosyltransferase; phosphoprotein; pyridoxal phosphate (Lys) (covalent) #status predicted									
F;820/Binding site: pyridoxal phosphate (Lys)									
Query Match									
C;Species: Solanum tuberosum (potato)									
C;Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004									
C;Accession: S53489; S34189									
R;Sonnewald, U.; Basner, A.; Greve, B.; Steup, M.									
Plant Mol. Biol. 27, 567-576, 1995									
A;Title: A second L-type isotype of potato glucan phosphorylase: cloning, antisense inhi									

Qy 3 DGPTLREWIISFC 14  
Db 619 NGVTPRRLWSRC 630

RESULT 3  
S00503 Na+/K+-exchanging ATPase (BC 3.6.3.9) alpha chain - Pacific electric ray  
C;Species: Torpedo californica (Pacific electric ray)  
C;Date: 30-Jun-1993 #sequence revision 30-Jun-1993 #text\_change  
C;Accession: S00503; S28885; S29880  
A;Title: Primary structure of the alpha subunit of Torpedo californica (Na(+)+K(+)) ATPase  
A;Reference number: S00503; MUID:2993905  
A;Accession: S00503  
A;Molecule type: mRNA  
A;Residues: 1-1022 <KAW1>  
A;Cross-references: UNIPROT:PO5025; EMBL:X02810; NID:964399; PIDN:CAA26578-1; PMID:964400  
A;Accession: S28885  
A;Molecule type: protein  
A;Residues: 228-240;431-438;535-550;671-690;1011-1022 <KAW2>  
R;Ohta, T.; Nagano, K.; Yoshida, M.  
Proc. Natl. Acad. Sci. U.S.A. 83, 2071-2075, 1986  
A;Title: The active site structure of Na(+)+K(+)-transporting ATPase: location of the 5'-  
A;Reference number: S29880; MUID:86177549; PMID:3008150  
A;Accession: S29880  
A;Molecule type: protein  
A;Residues: 386-402;502-512;671-689;887-906 <OHT>  
C;Supplementary: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain  
C;Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium trans-

F:56-120/Domain: transmembrane #status predicted <TM1>  
F:130-149/Domain: transmembrane #status predicted <TM2>  
F:150-280/Domain: intracellular #status predicted <INT1>  
F:291-313/Domain: transmembrane #status predicted <TM3>  
F:320-348/Domain: transmembrane #status predicted <TM4>  
F:349-785/Domain: intracellular #status predicted <INT3>  
F:587-783/Domain: ATPase nucleotide-binding domain homology <ATN>  
F:797-810/Domain: transmembrane #status predicted <TM5>  
F:849-874/Domain: intracellular #status predicted <INT6>  
F:895-932/Domain: transmembrane #status predicted <TM6>  
F:933-978/Domain: transmembrane #status predicted <TM7>  
F:979-1023/Domain: extracellular #status predicted <EXT>  
F:376/Active site: Asp (aspartyl)phosphate intermediate #status predicted  
F:508/Binding site: Asp (aspartyl)phosphate intermediate #status predicted  
F:717,721,726/Active site: Asp, Asp, Lys #status predicted  
F:716,720,725/Active site: Asp, Asp, Lys #status predicted  
Query Match 51.8% Score 44; DB 1; Length 1022;  
Best Local Similarity 70.0% Pred. No. 45; Mismatches 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 5 PTIREWISFC 14  
Db 84 PTIPEWIKFC 93

## RESULT 4

A24414 Na+/K+-exchanging ATPase (BC 3.6.3.9) alpha-1 chain - human  
N;Alternate names: sodium pump; sodium/potassium transporting ATPase alpha-A chain  
C;Species: Homo sapiens (man)  
C;Date: 02-Jun-1988 #sequence\_revision 02-Jun-1988 #text\_change 09-Jul-2004  
C;Accession: A24414; A27795; A3910; I60116; S09171  
R;Kawakami, K.; Ohta, T.; Nojima, H.; Nagano, K.  
J. Biochem. 100, 389-397, 1986  
A;Title: Primary structure of the alpha-subunit of human Na<sub>+</sub>K<sub>+</sub>-ATPase deduced from cDNA  
A;Reference number: A24414; MUID:87057096; PMID:2430951  
A;Accession: A24414  
A;Molecule type: mRNA  
A;Residues: 1-1023 <KAW2>  
A;Cross-references: UNIPROT:P05023; EMBL:X04297; NID:928926; PIDN:CAA27840.1; PMID:928927  
R;Shull, M.M.; Lingrel, J.B.  
Proc. Natl. Acad. Sci. U.S.A. 84, 4039-4043, 1987

## RESULT 5

T47701 translation initiation factor eIF-6-like protein [Imported] - *Arabidopsis thaliana*  
N;Alternate names: Protin Fl116.30  
C;Species: *Arabidopsis thaliana* (mouse-ear cress)  
C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
C;Accession: T47701  
R;Benes, V.; Wurmbrand, B.; Drzonek, H.; Ansorge, W.; Mewes, H.W.; Lemcke, K.; Mayer, K.F  
submitted to the Protein Sequence Database, March 2000  
A;Reference number: Z24473  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residue: 1-245 <ENTREZ>  
A;Cross-references: UNIPROT:Q9M060; EMBL:ALI61667  
A;Experiment source: cultivar Columbia; BAC clone Fl116  
C;Genetics:

A; Map position: 3  
 A; Introns: 4/1; 36/2; 65/1; 80/1; 123/3; 160/3  
 C; Superfamily: conserved hypothetical protein YPR016C  
 A; Note: Fl16.30

Query Match Score 43; DB 2; Length 245;  
 Best Local Similarity 50.6%; Pred. No. 17;  
 Matches 2; Mismatches 2; Indels 4; Gaps 0;

Qy 2 ADGPTURBWSFC 14  
 Db 194 AAGMTVNDWTSFC 206

## RESULT 6

To9084 phosphatidylinositol 3-kinase - Chlamydomonas reinhardtii (fragment)  
 C; Species: Chlamydomonas reinhardtii  
 C; Accession: T09084  
 C; Status: preliminary; translated from GB/EMBL/DBJ  
 A; Molecule type: DNA  
 A; Residues: 1-390 <MOL>  
 A; Cross-References: UNIPROT:004270; EMBL:U97663; NID:92109290; PIDN: AAC50018.1; PID:92109290  
 A; Experimental source: strain cw-15  
 C; Genetics: A; Introns: 265/3; 331/3; 370/3; 455/1; 481/3

## Query Match Score 43; DB 2; Length 490;

Best Local Similarity 57.1%; Pred. No. 32;  
 Matches 8; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

Qy 3 DGPTRLR-EWISFC 14  
 Db 250 DGSTARDEWLTCF 263

## RESULT 7

B37227 Na+/K+-exchanging ATPase (BC 3.6.3.9) alpha-3 chain - chicken  
 C; Species: Gallus gallus (chicken)  
 C; Accession: B37227; I50395  
 R; keyesay, K.; Lemas, V.; Fanbrrough, D. M.  
 Am. J. Physiol. 259, C619-C630, 1990  
 A; Title: Stability of Na(+)-K(+)-ATPase alpha-subunit isoforms in evolution.  
 A; Accession: A37227; M01D:91023019; PMID:2171348  
 A; Molecule type: mRNA  
 A; Residues: 1-1010 <TA2>  
 A; Cross-References: UNIPROT:P24798; GB: M5960; PID:9212407; PIDN: AAA48982.1; PID:9212408  
 C; Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain  
 C; Keywords: ATP; Glycoprotein; hydrolase; phosphoprotein; potassium transport; sodium transport  
 F; 574-770/Domain: ATPase nucleotide-binding domain homology <ATN>  
 F; 203-470/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F; 365/Active site: Asp (aspartyl)phosphate intermediate #status predicted  
 F; 495/Binding site: ATP (Lys) #status predicted

Query Match Score 43; DB 2; Length 1010;  
 Best Local Similarity 50.6%; Pred. No. 64;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 5 PTLEWISFC 14  
 Db 711 PTTPEWVKFC 83

## RESULT 8

Qy 5 PTLEWISFC 14  
 Db 711 PTTPEWVKFC 80

S00801 Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-3 chain - human  
 C; Species: Homo sapiens (man)  
 C; Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 09-Jul-2004  
 C; Accession: S00801; S0419; A2739; S02275  
 R; Ovchinnikov, Y.A.; Monastyrskaya, G.S.; Broude, N.E.; Melkov, A.M.; Smirnov, N.N.; Sverdlov, B.D.  
 FEBS Lett. 233, 87-94, 1988  
 A; Title: Family of human Na,K-ATPase genes. Structure of the gene for the catalytic subunit  
 A; Reference number: S00801; MUID:88255304; PMID:2838329  
 A; Accession: S00801  
 A; Molecule type: DNA  
 A; Residues: 1-1013 <OVC>  
 A; Cross-References: UNIPROT:P13637; EMBL:M37456  
 R; Sverdlov, B.D.; Monastyrskaya, G.S.; Broude, N.E.; Ushkarev, Y.A.; Melkov, A.M.; Smirnov, N.N.; Ovchinnikov, Y.A.  
 Dokl. Biochem. 297, 426-431, 1987  
 A; Title: Family of human Na(+)-K(+)-ATPase genes. Structure of the gene of isoform alpha  
 A; Reference number: S04019  
 A; Accession: S04019  
 A; Molecule type: DNA  
 A; Residues: 1-1013 <SVB1>  
 A; Cross-References: EMBL:X1210; NID:928963  
 A; Note: the authors translated the codon TTC for residue 283 as Ser and TCT for residue 284 as Cys. This paper is a translation of the Russian paper published in Dokl. Akad. Nauk SSSR, 1987, 297, 426-431.  
 A; Note: this paper is a translation of the Russian paper published in Dokl. Akad. Nauk SSSR, 1987, 297, 426-431.  
 A; Cross-References: EMBL:U97663; NID:92109290; PIDN: AAC50018.1; PID:92109290  
 A; Title: The family of human Na(+)-K(+)-ATPase genes. No less than five genes and/or pseudogenes. No less than five genes and/or pseudogenes. No less than five genes and/or pseudogenes.  
 A; Reference number: A27397; MUID:87247232; PMID:3036582  
 A; Accession: A27397  
 A; Molecule type: mRNA  
 A; Residues: 243-434 <SVB2>  
 A; Cross-References: GB:M27570  
 C; Genes:

A; Gene: GB:ATP1A3  
 A; Cross-References: GDB:119713; OMIM:182350  
 C; Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain  
 C; Keywords: ATP; heterodimer; hydrolase; ion transport; potassium transport  
 F; 86-110/Domain: transmembrane #status predicted <TM1>  
 F; 120-139/Domain: transmembrane #status predicted <TM1>  
 F; 140-280/Domain: intracellular #status predicted <INT2>  
 F; 283-305/Domain: transmembrane #status predicted <TM3>  
 F; 310-338/Domain: transmembrane #status predicted <TM4>  
 F; 339-774/Domain: transmembrane #status predicted <TM5>  
 F; 577-777/Domain: ATPase nucleotide-binding domain homology <ATN>  
 F; 777-800/Domain: transmembrane #status predicted <TM6>  
 F; 829-864/Domain: transmembrane #status predicted <TM7>  
 F; 865-942/Domain: intracellular #status predicted <INT4>  
 F; 943-968/Domain: transmembrane #status predicted <TM7>  
 F; 969-1013/Domain: extracellular #status predicted <EXT>  
 F; 365/Active site: Asp (aspartyl)phosphate intermediate #status predicted  
 F; 498/Binding site: ATP (Lys) #status predicted  
 F; 707,711,716/Active site: Asp, Asp, Lys #status predicted

Query Match Score 43; DB 1; Length 1013;  
 Best Local Similarity 60.0%; Pred. No. 64;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

## RESULT 9

C24539 Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-3 chain - rat  
 N; Alternate names: Na+/K+-transporting ATPase alpha (III) chain  
 C; Species: Rattus norvegicus (Norway rat)  
 C; Date: 30-Jun-1988 #sequence\_revision 23-Apr-1993 #text\_change 09-Jul-2004  
 C; Accession: C24633; S00514; B27180; A60470

R;Shull, G.E.; Greeb, J.; Lingrel, J.B.  
 A;Title: Molecular cloning of three distinct forms of the Na<sup>+</sup>,K<sup>+</sup>-ATPase alpha-subunit for  
 A;Reference number: A90512; MUID:3028408; PMID:3028400  
 A;Accession: C24639  
 A;Molecule type: mRNA  
 A;Residues: 1-1013 <SHU>  
 A;Cross-references: UNIPROT:PO06687; EMBL:MI4513; PIDN:AAA40777.1; PID:92030  
 A;Note: In the authors' translation 405-Ser is shown after residue 409 and, consequently  
 R;Fara, Y.; Urayama, O.; Wakamatsu, K.; Nojima, H.; Nagamune, H.; Ohta, T.; N  
 J. Biochem. 102, 3-58, 1987  
 A;Title: Primary structures of two types of alpha-subunit of rat brain Na<sup>+</sup>, K<sup>+</sup>-ATPase  
 A;Reference number: S00460; MUID:88032933; PMID:2822682  
 A;Accession: S00514  
 A;Molecule type: mRNA  
 A;Residues: 1-907, 'C', 909-1013 <HAR>  
 A;Cross-references: EMBL:05883; PID:955769; PIDN:CAA29307.1; PID:955770  
 R;Herrera, V.L.M.; Emanuel, J.R.; Ruiz-Opazo, N.; Levenson, R.; Nadal-Ginard, B.  
 J. Cell Biol. 105, 1855-1865, 1987  
 A;Title: Three differentially expressed Na<sup>+</sup>,K<sup>+</sup>-ATPase alpha subunit isoforms: structural and  
 A;Reference number: A22749; MUID:88033255; PMID:2822726  
 A;Accession: B27180  
 A;Molecule type: mRNA  
 A;Residues: 1, 'NL', 4-103, 'R', 105-113, 'E', 115-127, 'G', 129-148, 'Q', 150-151, 'T', 153-165, 'D'  
 A;Cross-references: EMBL:W28648; PIDN:g205633; PIDN:AAA41672.1; PID:920534  
 A;Note: The authors translated the codon CAG for residue 149 as Glu, GGC for residue 194  
 R;Hsu, Y.M.; Guido, G.  
 Biochemistry 28, 569-573, 1989  
 A;Title: Rat brain has the alpha3 form of the (Na<sup>+</sup>,K<sup>+</sup>)ATPase.  
 A;Reference number: A60470; MUID:89229049; PMID:2540801  
 A;Accession: A60470  
 A;Molecule type: protein  
 A;Residues: 117-112;586-595, 'X', 597-601 <HSU>  
 C;Comment: The alpha-3 form appears to be highly ouabain-inhibitable, as is alpha-2 but  
 C;Genetics: A;Gene: NRKAA3  
 C;Superfamily: Na<sup>+</sup>/K<sup>+</sup>-transporting ATPase nucleotide-binding domain  
 C;Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium transp  
 F;86-110/Domain: transmembrane #status predicted <TM1>  
 F;120-139/Domain: transmembrane #status predicted <TM2>  
 F;140-280/Domain: intracellular #status predicted <INT2>  
 F;281-303/Domain: transmembrane #status predicted <TM3>  
 F;310-338/Domain: transmembrane #status predicted <TM4>  
 F;339-776/Domain: intracellular #status predicted <INT3>  
 F;777-800/Domain: ATPase nucleotide-binding domain #status predicted <TM5>  
 F;839-864/Domain: transmembrane #status predicted <TM6>  
 F;943-968/Domain: intracellular #status predicted <INT4>  
 F;969-1013/Domain: extracellular #status predicted <EXT>  
 F;166/Active site: Asp (Asp) #status predicted <EXT>  
 F;498/Binding site: ATP (Lys) #status predicted <EXT>  
 F;707,711,716/Active site: Asp, Asp, Lys #status predicted  
 Query Match Score 43; DB 2; Length 1013;  
 Best Local Similarity 60.0%; Pred. No. 64;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 5 PTLEWISFC 14  
 DB 74 PTPEWVFC 83

RESULT 11

A;Accession: 150394  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-1017 <TAK>  
 A;Cross-references: UNIPROT:P24797; GB:MS5959; PIDN:9212405; PID:9212406  
 R;Takeyau, K.; Lemas, V.; Fambrough, D.M.  
 Am. J. Physiol. 259, C619-C630, 1990  
 A;Title: Stability of Na<sup>+</sup> K<sup>(+)</sup> ATPase alpha-subunit isoforms in evolution.  
 A;Reference number: A37227  
 A;Accession: A37227  
 A;Molecule type: mRNA  
 A;Residues: 3-1017 <TA2>  
 C;Superfamily: Na<sup>+</sup>,K<sup>+</sup>-transporting ATPase alpha chain - chicken  
 C;Species: Gallus gallus (chicken)  
 C;Date: 16-Sep-1992 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
 C;Accession: 150394; A37227  
 R;Takeyau, K.; Lemas, M.J.; Fambrough, D.M.  
 Am. J. Physiol. 259, 619-630, 1991  
 A;Title: Structure of the Na<sup>+</sup>,K<sup>+</sup>-ATPase alpha-subunit isoforms in evolution.  
 A;Reference number: 150394

Query Match 5 PTRENTSFC 14  
 Best Local Similarity 60.0%; Pred. No. 65; Indels 3; Gaps 0;  
 Matches 6; Conservative 1; Mismatches 1; Gaps 0;  
 Db 82 PTTPENVKFC 91

RESULT 12  
 B24639  
 B24639/Domain: ATPase nucleotide-binding domain homology <ATN>  
 P;784-807/Domain: transmembrane #status predicted <TM5>  
 P;846-871/Domain: transmembrane #status predicted <TM6>  
 P;872-949/Domain: intracellular #status predicted <INT4>  
 P;950-975/Domain: transmembrane #status predicted <TM7>  
 P;976-1020/Domain: intracellular #status predicted <EXT>  
 P;374/Active site: Asp (aspartylphosphate intermediate) #status predicted  
 P;505/Binding site: Asp, Asp, Lys #status predicted  
 P;714,18,73/Active site: Asp, Asp, Lys #status predicted

Query Match 5 PTRENTSFC 14  
 Best Local Similarity 60.0%; Pred. No. 65; Indels 3; Gaps 0;  
 Matches 6; Conservative 1; Mismatches 1; Gaps 0;  
 Db 82 PTTPENVKFC 91

RESULT 12  
 B24639  
 B24639/Domain: ATPase (EC 3.6.3.9) alpha-2 chain - rat  
 Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-2 chain - rat  
 Na+/K+-transporting ATPase alpha-plus chain  
 N;Alternate names: Na+/K+-transporting ATPase alpha-plus chain  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 30-Jun-1988 #sequence\_revision 30-Jun-1988 #text\_change 09-Jul-2004  
 C;Accession: B24639  
 R;Shull, G.B.; Green, J.; Lingrel, J.B.  
 Biochemistry 25, 8125-8132, 1986  
 A;Title: Molecular cloning of three distinct forms of the Na+, K+-ATPase alpha-subunit from rat heart  
 A;Reference number: A90512; MUID:87128908; PMID:3028470  
 A;Accession: B24639  
 A;Molecule type: mRNA  
 A;Residues: 1-1020 <SHU>  
 A;Cross-references: UNIPROT:PO6686; EMBL:ML14512; NID:920328; PID:920300

Query Match 5 PTRENTSFC 14  
 Best Local Similarity 60.0%; Pred. No. 65; Indels 3; Gaps 0;  
 Matches 6; Conservative 1; Mismatches 1; Gaps 0;  
 Db 82 PTTPENVKFC 91

RESULT 12  
 B24639  
 B24639/Domain: ATPase nucleotide-binding domain homology <ATN>  
 P;6-1020/Domain: Na+/K+-transporting ATPase alpha-2 chain #status predicted <ATN>  
 P;94-119/Domain: intracellular #status predicted <INT1>  
 P;128-147/Domain: transmembrane #status predicted <TM1>  
 P;289-311/Domain: intracellular #status predicted <TM2>  
 P;318-346/Domain: transmembrane #status predicted <TM3>  
 P;318-346/Domain: transmembrane #status predicted <TM4>  
 P;585-781/Domain: ATPase nucleotide-binding domain homology <ATN>  
 P;785-808/Domain: transmembrane #status predicted <TM5>  
 P;847-876/Domain: transmembrane #status predicted <TM6>  
 P;951-976/Domain: transmembrane #status predicted <TM7>  
 P;315/Binding site: cardiac Glycoside (Trp) #status predicted  
 P;506/Binding site: Asp (aspartylphosphate intermediate) #status predicted  
 P;506/Binding site: ATP (Lys) #status predicted

Query Match 5 PTRENTSFC 14  
 Best Local Similarity 60.0%; Pred. No. 65; Indels 3; Gaps 0;  
 Matches 6; Conservative 1; Mismatches 1; Gaps 0;  
 Db 82 PTTPENVKFC 91

RESULT 14  
 S04630  
 Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-1 chain - horse  
 C;Species: Equus caballus (domestic horse)  
 C;Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 09-Jul-2004  
 C;Accession: S04630  
 R;Kato, I.; Nagai, P.; Satoh, K.; Ushiyama, K.; Kano, K.  
 FEBS Lett. 250, 91-98, 1989  
 A;Title: Structure of the alpha(1) subunit of horse Na,K-ATPase gene.  
 A;Reference number: S04630; MUID:8929042; PMID:2544461  
 A;Accession: S04630  
 A;Molecule type: DNA  
 A;Residues: 1-1021 <KAN>  
 A;Cross-references: UNIPROT:PI18907; EMBL:X16773; NID:91010; PID:9871026

Query Match 5 PTRENTSFC 14  
 Best Local Similarity 60.0%; Pred. No. 65; Indels 3; Gaps 0;  
 Matches 6; Conservative 1; Mismatches 1; Gaps 0;  
 Db 82 PTTPENVKFC 91

RESULT 13  
 PWSHNA  
 Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain precursor - sheep  
 N;Alternate names: sodium pump alpha chain; sodium/potassium-dependent ATPase alpha chain  
 C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
 C;Accession: A01074; A35246  
 C;Date: 17-Mar-1987 #sequence\_revision 17-Mar-1987 #text\_change 09-Jul-2004  
 C;Accession: A01074; A35246  
 R;Shull, G.E.; Schwartz, A.; Lingrel, J.B.

F;951-976/Domain: transmembrane #status predicted <TM7>  
 F;977-1021/Domain: extracellular #status predicted <EXT>  
 P;374/Active site: Asp (aspartylphosphate intermediate) #status predicted  
 F;506/Binding site: ATP (Lys) #status predicted  
 F;715,719,724/Active site: Asp, Asp, Lys #status predicted  
  
 Query Match 50.6%; Score 43; DB 1; Length 1021;  
 Best Local Similarity 60.0%; Pred. No. 65;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
  
 Qy 5 PTLEWISFC 14  
 Db 82 PTPEWVKFC 91

RESULT 15  
 A28199  
 Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain - chicken  
 C;Species: Gallus gallus (chicken)  
 C;Accession: A28199  
 C;Cross-references: 21-Sep-1988 #sequence\_revision 21-Sep-1988 #text\_change 09-Jul-2004  
 R;Takeyasu, K.; Tamkun, M.M.; Renaud, K.J.; Fambrough, D.M.  
 J. Biol. Chem., 263, 437-4354, 1988  
 A;Title: Oubain-sensitive (Na<sup>+</sup>) + K<sup>(+)</sup>-ATPase activity expressed in mouse L cells by  
 A;Reference number: A28199; MUID:88153759; PMID:2831227  
 A;Accession: A28199  
 A;Status: preliminary; not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 1-1021 <TAK>  
 A;Cross-references: UNIPROT:P09572; GB:J03230; NID:9211219; PID:AAA48607.1; PID:g211220  
 C;Superfamily: Na<sup>+</sup>/K<sup>+</sup>-transporting ATPase alpha chain ATPase nucleotide-binding domain  
 C;Keywords: ATP; glycoprotein; hydrolase; phosphoprotein; transmembrane protein  
 F;565-761/Domain: ATPase nucleotide-binding domain homology <ATP>  
 F;213-481/Binding site: carbohydrate (An) (covalent) #status predicted  
 F;374/Active site: Asp (aspartylphosphate intermediate) #status predicted  
 F;506/Binding site: ATP (Lys) #status predicted  
  
 Query Match 50.6%; Score 43; DB 2; Length 1021;  
 Best Local Similarity 60.0%; Pred. No. 65;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
  
 Qy 5 PTLEWISFC 14  
 Db 82 PTPEWVKFC 91

Search completed: January 31, 2005, 18:22:36  
 Job time : 30 secs